

SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> LKB1 gene knock out animals

<130> C2-103PCT

<140>

<141>

<150> JP 1999-153030

<151> 1999-05-31

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 1795

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (51)..(1358)

<400> 1

aattcggatc caaggcggcc cgaaggacag aggacaaaga gtgggccagg atg gac 56

Met Asp

1

gtg gcg gac ccc gag ccg ttg ggc ctt ttc tcc gag ggc gag ctg atg 104

Val Ala Asp Pro Glu Pro Leu Gly Leu Phe Ser Glu Gly Glu Leu Met

5

10

15

tcg gtg ggc atg gac acc ttc atc cac cgc atc gac tcc acc gag gta 152

Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr Glu Val

20

25

30

atc tac cag ccg cgc cgc aaa cgc gcc aag ctc atc ggc aag tac ctg 200

Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys Tyr Leu

35

40

45

50

atg ggg gac ctg ctc ggg gag ggc tcg tac ggc aag gtg aag gag gtg 248

Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys Glu Val

55

60

65

ctg gac tcc gag acc tta tgc cgc agg gcg gtc aag atc ctc aag aag 296

Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu Lys Lys

70

75

80

aaa aag ctg cgc agg atc ccc aat gga gag gcc aac gtc aag aag gag 344

Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys Lys Glu

85

90

95

atc cag ctg ctg cgg cgg ctg cgg cat cgg aat gtg atc cag ctt gtg 392

Ile Gln Leu Leu Arg Arg Leu Arg His Arg Asn Val Ile Gln Leu Val

100

105

110

gac gtg ctg tac aat gag gag aag cag aag atg tat atg gtg atg gag 440

Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val Met Glu

115

120

125

130

tac tgc gta tgt ggc atg cag gag atg ctg gac agt gtg ccg gag aag 488

Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro Glu Lys

135

140

145

cgc ttc cct gtg tgc caa gct cat ggg tac ttc cgc cag ctg att gac 536

Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Arg Gln Leu Ile Asp

150

155

160

ggc ctg gaa tac cta cac agc cag ggc att gtt cac aag gac atc aag 584

Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp Ile Lys

165

170

175

ccg ggc aac ctg cta ctc acc acc aat ggc aca ctc aag atc tcc gac		632
Pro Gly Asn Leu Leu Leu Thr Thr Asn Gly Thr Leu Lys Ile Ser Asp		
180	185	190
ctc ggt gtt gcc gag gcc ctg cac cct ttc gct gtg gat gac acc tgc		680
Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Val Asp Asp Thr Cys		
195	200	205
cgg aca agc cag ggc tcc ccg gcc ttc cag cct cct gag att gcc aat		728
Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile Ala Asn		
215	220	225
gga ctg gac acc ttt tca ggt ttc aag gtg gac atc tgg tca gct ggg		776
Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser Ala Gly		
230	235	240
gtc aca ctt tac aac atc acc acg ggc ctg tac cca ttt gag ggg gac		824
Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu Gly Asp		
245	250	255
aat atc tac aag ctc ttt gag aac att ggg aga gga gac ttc acc atc		872
Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Arg Gly Asp Phe Thr Ile		
260	265	270
cct tgt gac tgc ggc cca cca ctc tct gac cta ctc cga ggg atg ttg		920
Pro Cys Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Arg Gly Met Leu		

275

280

285

290

gag tat gag ccg gcc aag agg ttc tcc atc cga cag att agg cag cac 968

Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg Gln His

295

300

305

agc tgg ttc cgg aag aaa cac cct ctg gct gag gcg ctc gta cct atc 1016

Ser Trp Phe Arg Lys Lys His Pro Leu Ala Glu Ala Leu Val Pro Ile

310

315

320

cca cca agc cca gac act aag gac cgc tgg cgc agt atg act gta gtg 1064

Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr Val Val

325

330

335

ccc tac ctg gag gac ctg cat ggc cgt gcg gag gag gag gag gaa 1112

Pro Tyr Leu Glu Asp Leu His Gly Arg Ala Glu Glu Glu Glu Glu

340

345

350

gac ttg ttt gac att gag gac ggc att atc tac acc cag gac ttc aca 1160

Asp Leu Phe Asp Ile Glu Asp Gly Ile Ile Tyr Thr Gln Asp Phe Thr

355

360

365

370

gtg cct gga cag gtc ctg gaa gag gaa gtg ggt cag aat gga cag agc 1208

Val Pro Gly Gln Val Leu Glu Glu Val Gly Gln Asn Gly Gln Ser

375

380

385

cac agt ttg ccc aag gct gtt tgt gtg aat ggc aca gag ccc cag ctc 1256

His Ser Leu Pro Lys Ala Val Cys Val Asn Gly Thr Glu Pro Gln Leu

390

395

400

agc agc aag gtg aag cca gaa ggc cga cct ggc acc gcc aac cct gcg 1304

Ser Ser Lys Val Lys Pro Glu Gly Arg Pro Gly Thr Ala Asn Pro Ala

405

410

415

cgc aag gtg tgc tcc agc aac aag atc cgc cggtc tcg gcc tgc aag 1352

Arg Lys Val Cys Ser Ser Asn Lys Ile Arg Arg Leu Ser Ala Cys Lys

420

425

430

cag cag tgactgaggc ctacagtgtg tcatcaggat ctctggcag gtgtccctgc 1408

Gln Gln

435

aaggctgggt ttccaggcc tgcctgtcca ctcacttcgg gacgttggag ccgagggcgg 1468

acctgctgcc ccagaagcac ttatgtcga gaccactggc cggcattgcc tgcattccgc 1528

cctgcgagcc tcgctgtctt tgggttggtt tcttttttttaataaaaaca ggtggatttg 1588

agctatggct atgagggtgt ttggaaatat ggagcaggcg gggcacaggg tggcctgcag 1648

agaaaaccag agcaaacaaa tatgcagaga catttatgtat taaccagaca acacgaccaa 1708

ccacagaggg cgcaaggcag ggagtggca ggcactaca gcgagtctgc cctatcttt 1768

ggcaataaat aaagcttggg aaacttg 1795

<210> 2

<211> 436

<212> PRT

<213> Mus musculus

<400> 2

Met Asp Val Ala Asp Pro Glu Pro Leu Gly Leu Phe Ser Glu Gly Glu

1	5	10	15
---	---	----	----

Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr

20	25	30
----	----	----

Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys

35	40	45
----	----	----

Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys

50	55	60
----	----	----

Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu

65	70	75	80
----	----	----	----

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys

85

90

95

Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Arg Asn Val Ile Gln

100

105

110

Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val

115

120

125

Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro

130

135

140

Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Arg Gln Leu

145

150

155

160

Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp

165

170

175

Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Asn Gly Thr Leu Lys Ile

180

185

190

Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Val Asp Asp

195

200

205

Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile

210

215

220

Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
225 230 235 240

Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
245 250 255

Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Arg Gly Asp Phe
260 265 270

Thr Ile Pro Cys Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Arg Gly
275 280 285

Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
290 295 300

Gln His Ser Trp Phe Arg Lys Lys His Pro Leu Ala Glu Ala Leu Val
305 310 315 320

Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
325 330 335

Val Val Pro Tyr Leu Glu Asp Leu His Gly Arg Ala Glu Glu Glu
340 345 350

Glu Glu Asp Leu Phe Asp Ile Glu Asp Gly Ile Ile Tyr Thr Gln Asp

355

360

365

Phe Thr Val Pro Gly Gln Val Leu Glu Glu Val Gly Gln Asn Gly

370

375

380

Gln Ser His Ser Leu Pro Lys Ala Val Cys Val Asn Gly Thr Glu Pro

385

390

395

400

Gln Leu Ser Ser Lys Val Lys Pro Glu Gly Arg Pro Gly Thr Ala Asn

405

410

415

Pro Ala Arg Lys Val Cys Ser Ser Asn Lys Ile Arg Arg Leu Ser Ala

420

425

430

Cys Lys Gln Gln

435

<210> 3

<211> 5876

<212> DNA

<213> Mus musculus

<220>

<221> exon

<222> (1)..(84)

<220>

<221> intron

<222> (85)..(677)

<220>

<221> exon

<222> (678)..(767)

<220>

<221> intron

<222> (768)..(1231)

<220>

<221> exon

<222> (1232)..(1364)

<220>

<221> intron

<222> (1365)..(1431)

<220>

<221> exon

<222> (1432)..(1568)

<220>

<221> intron

<222> (1569)..(1852)

<220>

<221> exon

<222> (1853)..(1980)

<220>

<221> intron

<222> (1981)..(2243)

<220>

<221> exon

<222> (2244)..(2301)

<220>

<221> intron

<222> (2302)..(3102)

<220>

<221> exon

<222> (3103)..(3299)

<220>

<221> intron

<222> (3300)..(5103)

<220>

<221> exon

<222> (5104)..(5310)

<220>

<221> intron

<222> (5311)..(5454)

<220>

<221> exon

<222> (5455)..(5876)

<400> 3

ggagatccag ctgctgcggc ggctgcccga tcgaaatgtg atccagcttg tggacgtgct 60

gtacaatgag gagaaggcaga agatatatcc tgtgggtgga gtgggctggg gtggccctg 120

tgttagggc tggaaggcctt ctgcaaggcc tctggcagca atagtgtac atgtcatcct 180

gtggcgcctg tcagctcatc aggcagggga gcaaggcatg gggcttcac ctggcgccag 240

cctgttctga gcagtgtggc tggactggg catggcctca cagggacttg gggctatgt 300

acattgacag ggccccggct ggttcttagag gttccatgc tgcccttcc cagaggtaga 360

ggttgcacag cctacgttgc atctggcag tcctgggagc attctgagaa cccagtgcc 420

tgcagccccca actcctggta cccatctctc cctgtggcta gtacaccagc tgatttcagt 480

cctgttgtaa tctatgctga ctccatgtgg tccaagtcac tgtggtggtc ttgtggaccc 540

tgtgagttact gatagggagc gcagaatggc gggagagcag agtggtggtg gtctgttggc 600

ccagcggggc cctccagacc actgttgcta ggagcaggc tcctggcctt ggtgtgctgc 660

tttccttagc gccctacgta tatggtgatg gagtactgcg tatgtggcat gcaggagatg 720

ctggacagtg tgccggagaa gcgcctccct gtgtgccaag ctcatgggtg agtgcctgc 780

tgggtgcagg aggagcagcc attgtcagga aaccagggtg tttctggcc cccagtttt 840

aaccaggcca atgtgcttag ggttaccctc ttgttaggcc ctgtggccc gtcgcctgc 900

agagccatag tgggtctgag tcctgttcag tgctcccagg ttcagcagaa tcacatcccc 960

tggtagcag agaacaaagg gaaggaaagg gaaggaagca agccagaggg gaaacctggc 1020

tccctggcc tggcagcag tgactgccag ttgccctgtg taattttagt ggcccagcct 1080

tctgactctc aggtctgtt gcctgagccc taaacatcta tcaccttgta ggccaggtct 1140

catgagtctc ccaaacttca tatcagactt atgttaggtac catggtatgg gctgagacac 1200

tgtggggcct gagccagtcc cacccattca ggtacttccg ccagctgatt gacggcctgg 1260

aataacctaca cagccaggc attgttcaca aggacatcaa gccggcaac ctgctactca 1320

ccaccaatgg cacactcaag atctccgacc tcggtgttgc cgaggttaggc accatgtgca 1380

gggatcatgg gccgcttctc ctgagctgcc ctgactctca ctgccctgca ggccctgcac 1440

ccttcgctg tggatgacac ctgccggaca agccagggct ccccgccct ccagcctcct 1500

gagattgcca atggactgga cacctttca ggttcaagg tggacatctg gtcagctggg 1560

gtcacactgt aagtgtctt ttttgcctt gtagcagatg gggggctgtg gttttccct 1620

agtgttcttg ggccttttg cccacagtgt gtggctagca ggttggacat tccaggtctg 1680

tgggtgtgg ttcctaccct accccacccc actccacagg gttttgttg cacacagatg 1740

taggtgccat gactgcacat ctaccagtttta acatgtgtcc tgtctggag ttggggcacc 1800

tgtcctctgg tctccagtgt ggccagcact gacactctt tcctatgtga agttacaaca 1860

tcaccacggg cctgtaccca tttgaggggg acaatatcta caagctctt gagaacattg 1920

ggagaggaga cttcaccatc cttgtgact gcggcccacc actctctgac ctactccgag 1980

gtgggcatct ctaaatcacc caaatgttag gacagcaagg gacagagccc ctggtctgga 2040

ggggttctga ctttactgtc aggacagcct ttgtccgcca gatgggagg tttctgagat 2100

tgcttcccc catctgggc cgggtgggt gggtgggtc tcagtctat gggcctagg 2160

aaggccaagg gatggatgc tgttagtggtg ctgtacaca aacaggcac ctgctacact 2220

cacttatctc ttctgtccta cagggatgtt ggagtatgag ccggccaaga gtttctccat 2280

ccgacagatt aggcagcaca ggtgaggcatg gccggcctgt ctcagectgc tgggggtctg 2340

agctgagaac atggtctcag aggtgctagg tcatcacagg agtaaggatc agtgtgctgt 2400

gtgtatttgc gtctggaaag gctgtgtgt aacttgggt gtgacagggg tgcccaatgc 2460

aggcctccct acctttatca ttttgttcag gagtgcaggc gttatgtggc ctgagaagct 2520

gttagatttca gggcttagaa ttagagacgg atcctccat ggtggggagg gaggagtaga 2580

tggggaaatgt tcactttgga tcccaatgt tccttggcca tctggacatg gaaatgtgtc 2640

tagggaggcc aacaggaagc gtgaggcatg gtgtcttcc tcacctgagg ctaagagcct 2700

tctggtaac agtggagcct ctgtcctccc tttgttatt taccagctgg tcagagcctt 2760

tgggtccagg cttctctgtc ctcttcctcc ttcatgctag actgagactg gctcagctgg 2820

gtgtccccca gtgagggctt ctagcctatc cgtgttcaag gcgggtggga ctatagggtgc 2880

agggacctga ttgcccaccc tagtccaagg cgctgtggct gtcatacgatg ggtggtggtt 2940

tgtgccagtg ctatgggtgt taggctacct caagcctgtta gccggagcac taaggcctcg 3000

tcttatgtaa ggacagccat ggtgtggct ttgggtggta ttggccagcc gtggtcacag 3060

tgcctggcac ctgatgtctg tgctgcactt ggccttcattt agctggttcc ggaagaaaaca 3120

ccctctggct gaggcgctcg tacctatccc accaagccca gacactaagg accgctggcg 3180

cagtatgact gtagtgcctt acctggagga cctgcattggc cgtgcggagg aggaggagga 3240

ggaagacttg tttgacattt aggacggcat tatctacacc caggacttca cagtgcctgg 3300

taagctggct tggcgccagct cctactggag ctgggtactt tgtgcactct ggggctggtc 3360

cccttcccaa gtctccagcc agctaacatg agccaccagg actgccaaag ccattctgggt 3420

ggctgtggca tttcactctg ggcttagatga agggctccct ggctgcattt agcaggagga 3480

gggaaacct ggagggcagt ggtaggggc cctgagacag ccacctgagg gagggtccag 3540

tggccctcggttc tcctggccat gcctgaccctt atatgcctt cttccccagg tgtcgaggag 3600

gcggccgagg cagggcttag cgaggatgca tgcgacacat gcatgtggaa gagccaggc 3660

gcaggccttc ctggagagga gcccgaggag gggtttgggg cttagtgta gctccctgtc 3720

tgctgcccca cccatgtcct ccataaagct ttgtccactg tgtctgcagg tggatgctt 3780

ccgcgacttc ctcctgtca ctaccctgac aggctccccca ccagggttc agagaacatg 3840

cctgggtcca aggctgagc taggtcctca gtgccagggt ggccaccagc caggggctct 3900

tggggcctt gttcctgtgg cctgcatgcc agtcccactt agtcctggc cttcaaata 3960

gcttggtgg gagggtaagg accttggct actgtgtctc ctgttagcaat tgagagttct 4020

aatagcagtg cccgctgggt gccaggtgga atccacaagg acaggtatac acctgatgtc 4080

cagtatggc cttggccaca gccctttcta aggttaaag catccctatg tggaatagt 4140

gtcttctact ctgtcacgtg gagcccttgt ctagactgtc ccacaggctg ggctcctggc 4200

tgagagctgg tttctctgct ggggagaaga tgtacttagg tgctgggtgc atgagggacc 4260

cttaaggctg ctgtggttt aaggaaggca agggtctgg gacactggtt gccatggag 4320

cccatttgtc aaatgggta gtgtgcaca gagtgaagt accgtgctc gaggatagcc 4380

tgatccctct gtacttggca tgagggtcgg actctgcagc aacaggacag gggcttcta 4440

ctcagtcct tgtgtggagg agggacaga tgcttctca gagtccacct gacctcaagc 4500

ctcagtccca tgcagagtga gccagagtgg gtgctgctag tgtggccaag tcagagggtt 4560

tgggagagaa attctggatc caggagcgtg ggcagtggc tgtgtgctgg gttccacagc 4620

cgcattgcca agcactggac tgtggagtt catgtagaca ctgacctctg gaggctggga 4680

agttcagga gaggccatct ttgtccac tgcgagggca ggccaacaga gcaagctgg 4740

ctgcagccct cagctggatg atctccttcc cggtgctcat cgtagctagt agtcccagg 4800

ccgaatgctt cattccttg tgcctgtact gaggtcttag agcctctccc ttggagagct 4860

ctgtgagctg gtgctggct gcccaggcta gacaggcagg tgagcgtgg catgctgcag 4920

gagggccagg gcatagcact gtgaaggcag tggcctgct tgccttgga gctactgagg 4980

ggtgtggtgcc accagaggct agagcaccc cgaccagcct ctgtcacagt tgggctggc 5040

tgggccctgg ggctttgagc tacctgcccc ttggctcaag ctatgcttgc catcttcccg 5100

taggacaggt cctggaagag gaagtgggtc agaatggaca gagccacagt ttgcccagg 5160

ctgtttgtgt gaatggcaca gagccccagc tcagcagcaa ggtgaagcca gaaggccgac 5220

ctggcacccgc caaccctgcg cgcaagggtgt gctccagcaa caagatccgc cggctctcgg 5280

cctgcaagca gcagtgactg aggctacag gtgggcatgg gcctgggtcc agccatccct 5340

ggtgttcaca gtgggtgtct gctgggctcc tagtccttc ccgttagggca gtgctgcaag 5400

gggaaaggc tggtggttga ggtggtacta agtgaccacc cattctacca acagtgtgtc 5460

atcaggatct ctggcaggt gtccctgcaa ggctgggttt tccaggcctg cctgtccact 5520

cacttcggga cgttggagcc gagggcggac ctgctgcccc agaagcactt tatgtcgaga 5580

ccactggccg gccttgcctg catgccccc tgcgagcctc gctgtcttg gttggtttc 5640

tttttttta ataaaacagg tggattttag ctatggctat gaggggtttt gaaaaatatgg 5700

agcaggcggg gcacagggtg gcctgcagag aaaacccaga gcaaacaat atgcagagac 5760

atttatgatt aaccagacaa cacgaccaac cacagagggc gcagggcagg gagtggcag 5820

gcactcacag cgagtctgcc ctatctttg gcaataaata aagctggga aacttg 5876

<210> 4

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 4

gatgaattcc gaaggacaga ggacaaagag tgg 33

<210> 5

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 5

gatgaattct tagaggtctt cttctgagat gagcttctgc tcctgctgct tgcaggccga 60

<210> 6

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 6

tgcgcagctt ttttttttg agga 24

<210> 7

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 7

ggtgatggag tactgcgtgt g

21

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 8

ggtgaagtct cctctcccaa tgg

24

<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 9

actgcagctg acccaagcca ggat

24

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 10

cgaaggacag aggacaaaga gtgg

24

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 11

tgcgacacat cgataccgct cgagtcg

27

<210> 12

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 12

aattcgactc gagcggtatc gatgtgtcgc atgca

35

<210> 13

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 13

ctagtcaagc ttcataactt cgtatagcat acattatacg aagttatcga attcgacctg 60

gatccataa cttcgtatag catacattat acgaagttat caagcttcc 109

<210> 14

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 14

tcgaggaagc ttgataactt cgtataatgt atgctatacg aagttatggg atccaggtcg 60

aattcgataa cttcgtataa tgtatgctat acgaagttat gaagcttga 109

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Linker Sequence

<400> 15

gatgttccac ctcgagccca ggctccagag gtcagt

36

<210> 16

<211> 86

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 16

gatctcgaga tcgatggtag cggtgttcca cataacttcg tatagcatac attatacgaa 60

gttatctgtc cactgtgtct gcaggt

86

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 17

ccgggtttcc acataacttc

20

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 18

gtttcccaag ctttatttat tgcc

24

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 19

cagcagcaag gtgaagccag aagg

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 20

cctttggctg ctgggtgact tctg

24

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 21

acagagctct ccaagggaga 20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 22

ctctcccaaa ccctctgact 20